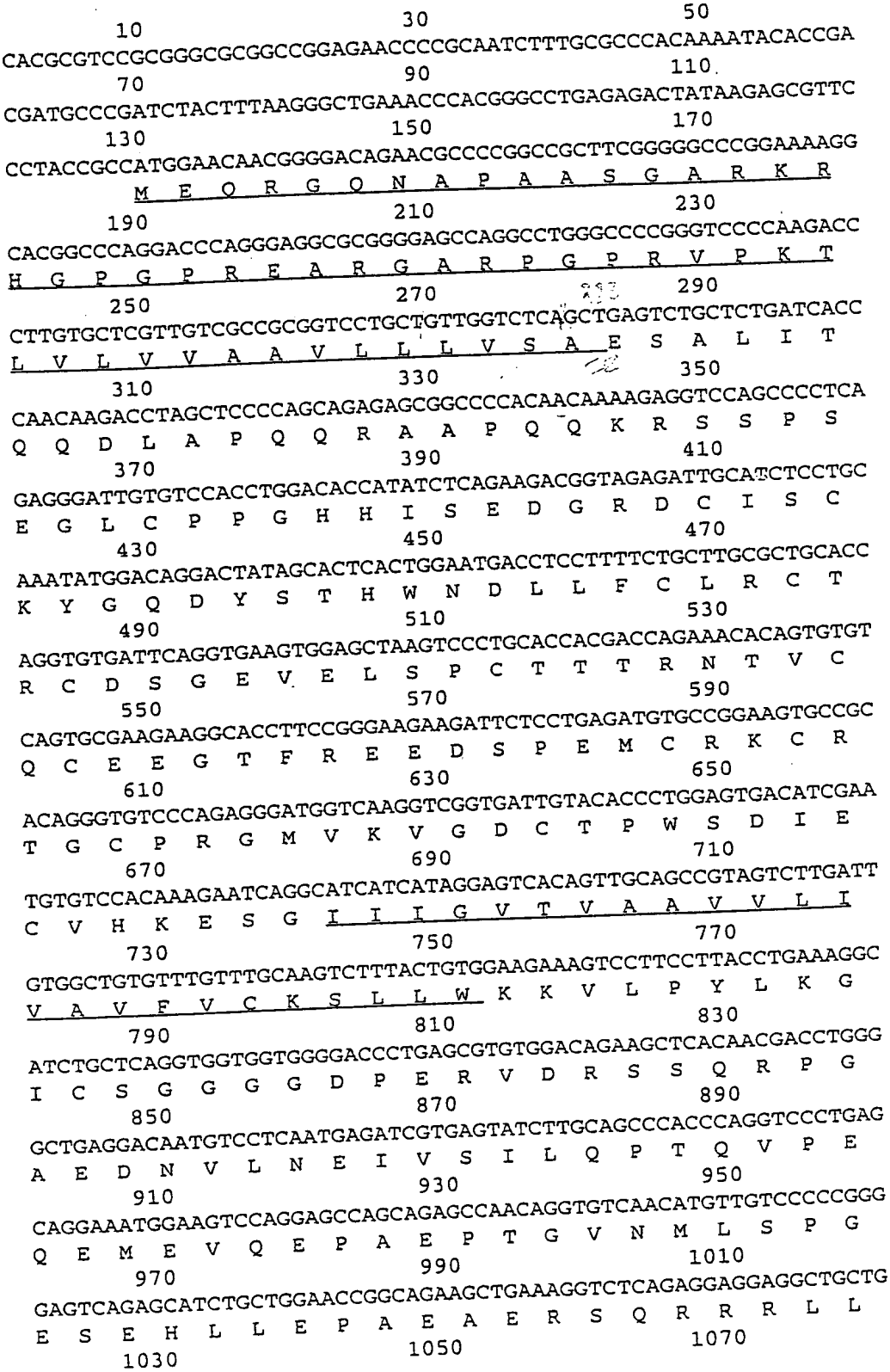
Figure 1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30
50
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70
90
110
CGATGCCCGATCTACTTTAAGGGCTGAAACCCACGGGCCTGAGAGACTATAAGAGCGTTC
130
150
170
CCTACCGCCATGGAACAACGGGGACAGAACGCCCCGGCCGCTTCGGGGGCCCGGAAAAGG
M E Q R G Q N A P A A S G A R K R
190
210
230
CACGGCCCAGGACCCAGGGAGGCGCGGGGAGCCAGGCCTGGGCCCCGGGTCCCCAAGACC
H G P G P R E A R G A R P G P R V P K T
250
270
290
CTTGTGCTCGTTGTCGCCGCGGTCCTGCTGTTGGTCTCAGCTGAGTCTGCTCTGATCACC
L V L V V A A V L L L V S A E S A L I T
310
330
350
CAACAAGACCTAGCTCCCCAGCAGAGAGCGGCCCCACAACAAAAGAGGTCCAGCCCCTCA
Q Q D L A P Q Q R A A P Q Q K R S S P S
370
390
410
GAGGGATTGTGTCCACCTGGACACCATATCTCAGAAGACGGTAGAGATTGCATCTCCTGC
E G L C P P G H H I S E D G R D C I S C
430
450
470
AAATATGGACAGGACTATAGCACTCACTGGAATGACCTCCTTTTCTGCTTGCGCTGCACC
K Y G Q D Y S T H W N D L L F C L R C T
490
510
530
AGGTGTGATTCAGGTGAAGTGGAGCTAAGTCCCTGCACCACGACCAGAAACACAGTGTGT
R C D S G E V E L S P C T T T R N T V C
550
570
590
CAGTGCGAAGAAGGCACCTTCCGGGAAGAAGATTCTCCTGAGATGTGCCGGAAGTGCCGC
Q C E E G T F R E E D S P E M C R K C R
610
630
650
ACAGGGTGTCCCAGAGGGATGGTCAAGGTCGGTGATTGTACACCCTGGAGTGACATCGAA
T G C P R G M V K V G D C T P W S D I E
670
690
710
TGTGTCCACAAAGAATCAGGCATCATCATAGGAGTCACAGTTGCAGCCGTAGTCTTGATT
C V H K E S G I I I G V T V A A V V L I
730
750
770
GTGGCTGTGTTTGTTTGCAAGTCTTTACTGTGGAAGAAAGTCCTTCCTTACCTGAAAGGC
V A V F V C K S L L W K K V L P Y L K G
790
810
830
ATCTGCTCAGGTGGTGGTGGGGACCCTGAGCGTGTGGACAGAAGCTCACAACGACCTGGG
I C S G G G G D P E R V D R S S Q R P G
850
870
890
GCTGAGGACAATGTCCTCAATGAGATCGTGAGTATCTTGCAGCCCACCCAGGTCCCTGAG
A E D N V L N E I V S I L Q P T Q V P E
910
930
950
CAGGAAATGGAAGTCCAGGAGCCAGCAGAGCCAACAGGTGTCAACATGTTGTCCCCCGGG
Q E M E V Q E P A E P T G V N M L S P G
970
990
1010
GAGTCAGAGCATCTGCTGGAACCGGCAGAAGCTGAAAGGTCTCAGAGGAGGAGGCTGCTG
E S E H L L E P A E A E R S Q R R R L L
1030
1050
1070

Figure 1 (continued)

GTTCCAGCAAATGAAGGTGATCCCACTGAGACTCTGAGACAGTGCTTCGATGACTTTGCA

V P A N E G D P T E T L R Q C F D D F A

1090 1110 1130

GACTTGGTGCCCTTTGACTCCTGGGAGCCGCTCATGAGGAAGTTGGGCCTCATGGACAAT

D L V P F D S W E P L M R K L G L M D N

1150 1170 1190

GAGATAAAGGTGGCTAAAGCTGAGGCAGCGGGCCACAGGGACACCTTGTACACGATGCTG

E I K V A K A E A A G H R D T L Y T M L

1210 1230 1250

ATAAAGTGGGTCAACAAAACCGGGCGAGATGCCTCTGTCCACACCCTGCTGGATGCCTTG

I K W V N K T G R D A S V H T L L D A L

1270 1290 1310

GAGACGCTGGGAGAGAGACTTGCCAAGCAGAAGATTGAGGACCACTTGTTGAGCTCTGGA

E T L G E R L A K Q K I E D H L L S S G

1330 1350 1370

AAGTTCATGTATCTAGAAGGTAATGCAGACTCTGCCATGTCCTAAGTGTGATTCTCTTCA

K F M Y L E G N A D S A M S *

1390 1410 1430

GGAAGTGAGACCTTCCCTGGTTTACCTTTTTCTGGAAAAAGCCCAACTGGACTCCAGTC

1450 1470 1490

AGTAGGAAAGTGCCACAATTGTCACATGACCGGTACTGGAAGAAACTCTCCCATCCAACA

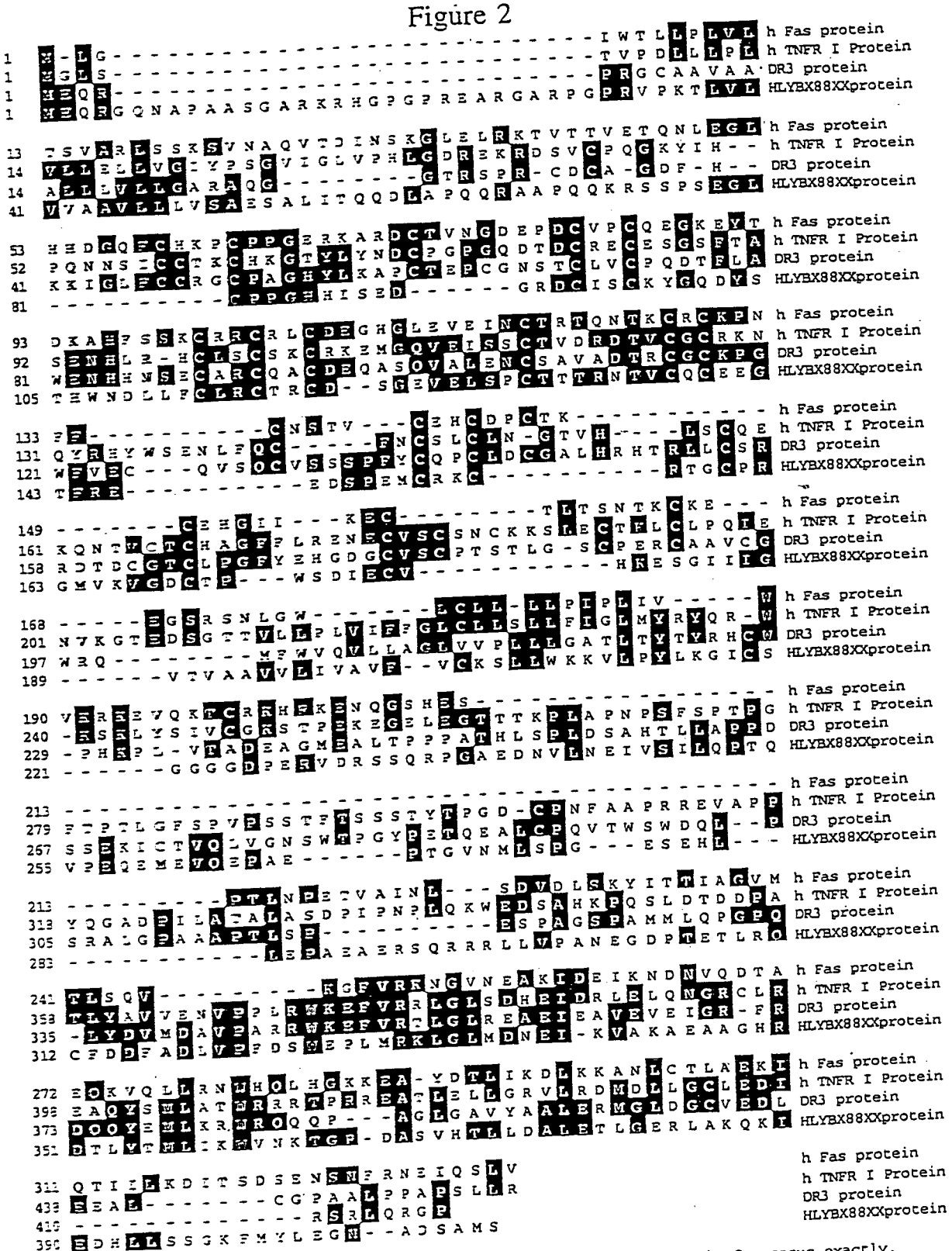
1510 1530 1550

TCACCCAGTGGATGGAACATCCTGTAACTTTTCACTGCACTTGGCATTATTTTTATAAGC

1570 1590

TGAATGTGATAATAAGGACACTATGGAAAAAAAAAAAAAA

Figure 2



Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

Figure 3

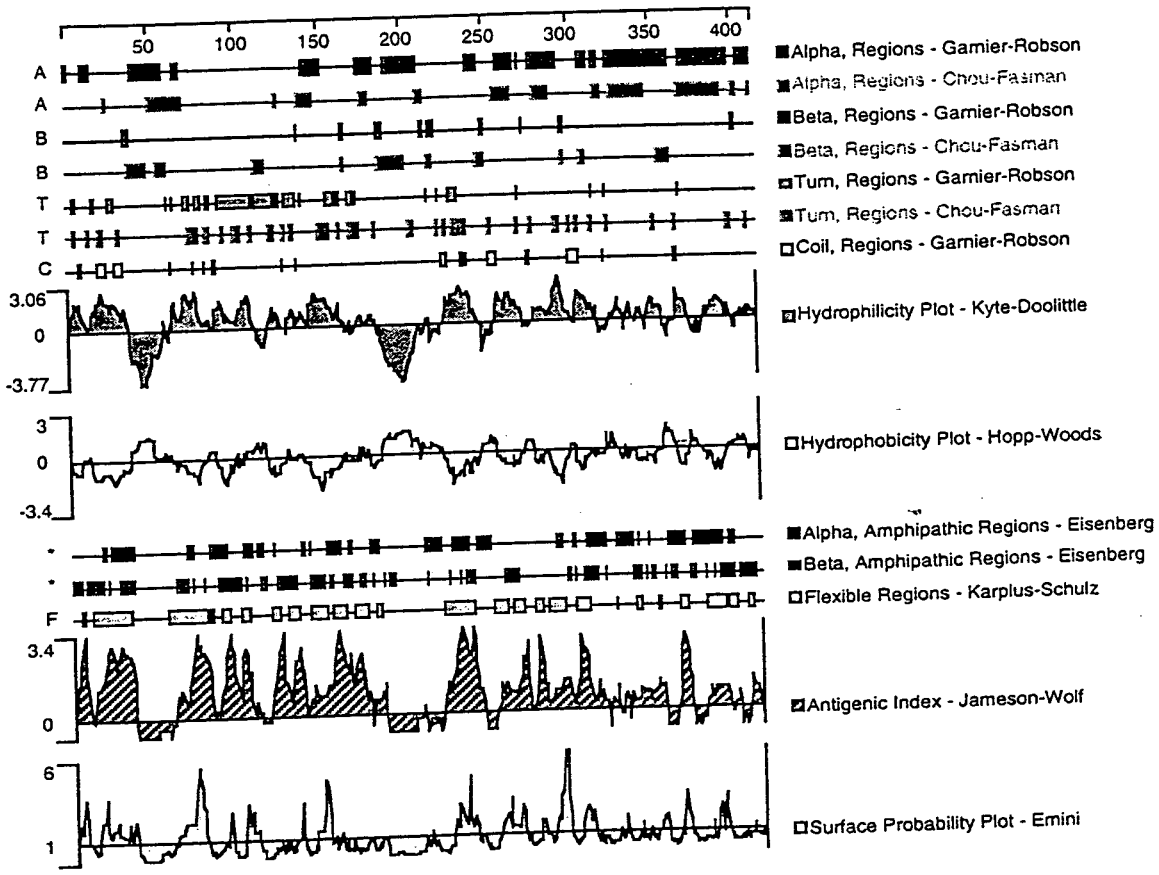

50
100
150
200
250
300
350
400
A
A
B
B
T
T
C
3.06
0
-3.77
3
0
-3.4
*
*
F
3.4
0
6
1
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
Hydrophilicity Plot - Kyte-Doolittle
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
Antigenic Index - Jameson-Wolf
Surface Probability Plot - Emini

Figure 4

HAPBU13R

```
  1 AATTCGGCAC AGCTCTTCAG GAAGTCAGAC CTTCCCTGGT TTACCTTTTT
 51 TCTGGAAAAA GCCCAACTGG GACTCCAGTC AGTAGGAAAG TGCCACAATT
101 GTCACATGAC CGGTACTGGA AGAAACTCTC CCATCCAACA TCACCCAGTG
151 GNATGGGAAC ACTGATGAAC TTTTCACTGC ACTTGGCATT ATTTTTGTNA
201 AGCTGAATGT GATAATAAGG GCACTGATGG AAATGTCTGG ATCATTCCGG
251 TTGTGCGTAC TTTGAGATTT GNGTTTGGGG ATGTNCATTG TGTTTGACAG
301 CACTTTTTTN ATCCCTAATG TNAAATGCNT NATTTGATTG TGANTTGGGG
351 GTNAACATTG GTNAAGGNTN CCCNTNTGAC ACAGTAGNTG GTNCCCGACT
401 TANAATNGNN GAANANGATG NATNANGAAC CTTTTTTTGG GTGGGGGGGT
451 NNCGGGGCAG TNNAANGNNG NCTCCCCAGG TTTGGNGTNG CAATNGNGGA
501 ANNNTGG
```

HSBBU76R

```
  1 TTTTTTTTGT AGATGGATCT TACAATGTAG CCCAAATAAA TAAATAAAGC
 51 ATTTACATTA GGATAAAAAA GTGCTGTGAA AACAATGACA TCCCAAACCA
101 AATCTCAAAG TACGCACAAA CGGAATGATC CAGACATTTC CATAGNGTCC
151 TTATTATCAC ATTCAGCTTA TAAAANTAAT GCCAAGTGCA GTGAAAAGTT
201 ACAGGATGTT CCATCCACTG GGTGGATT
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Figure 5

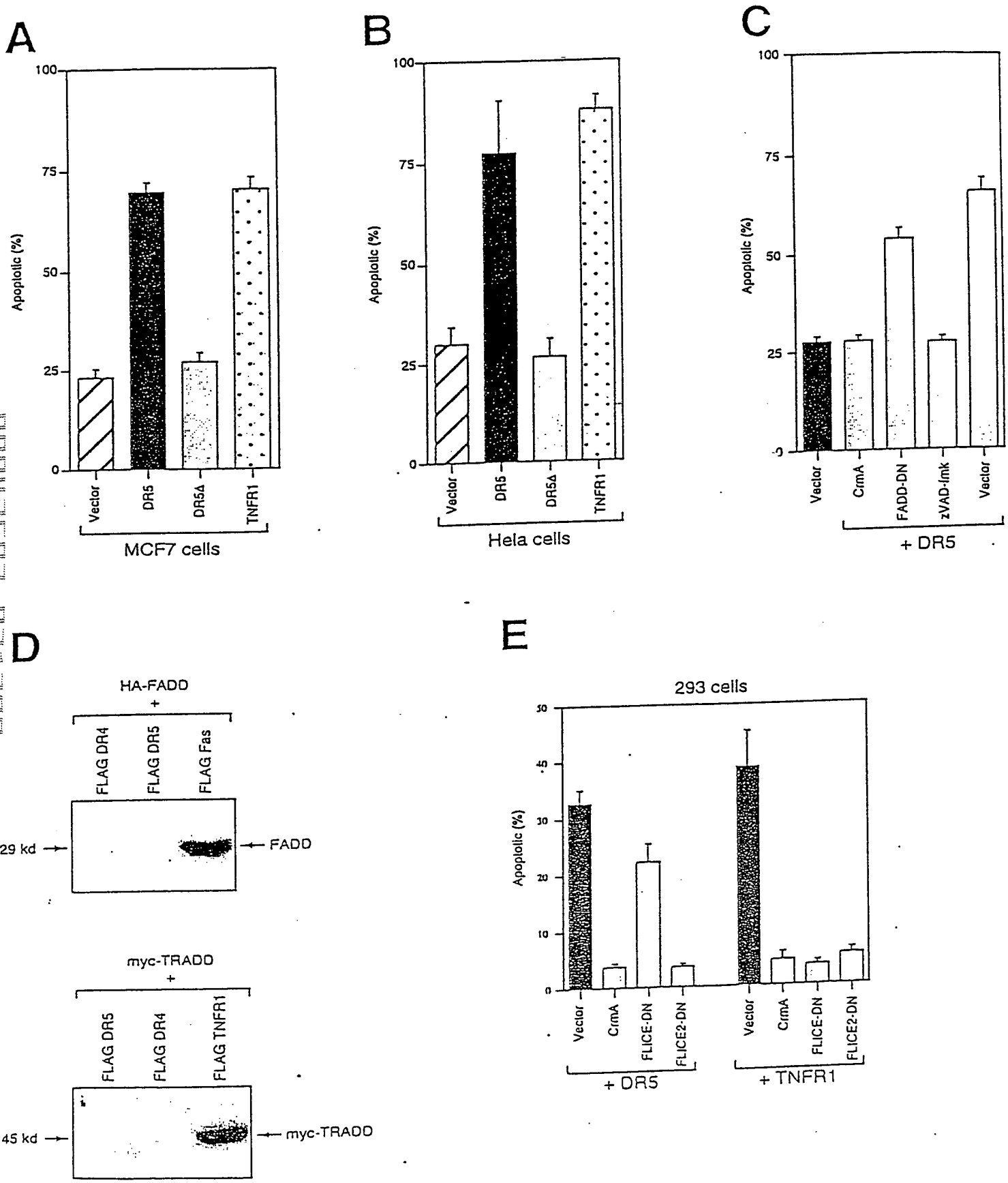
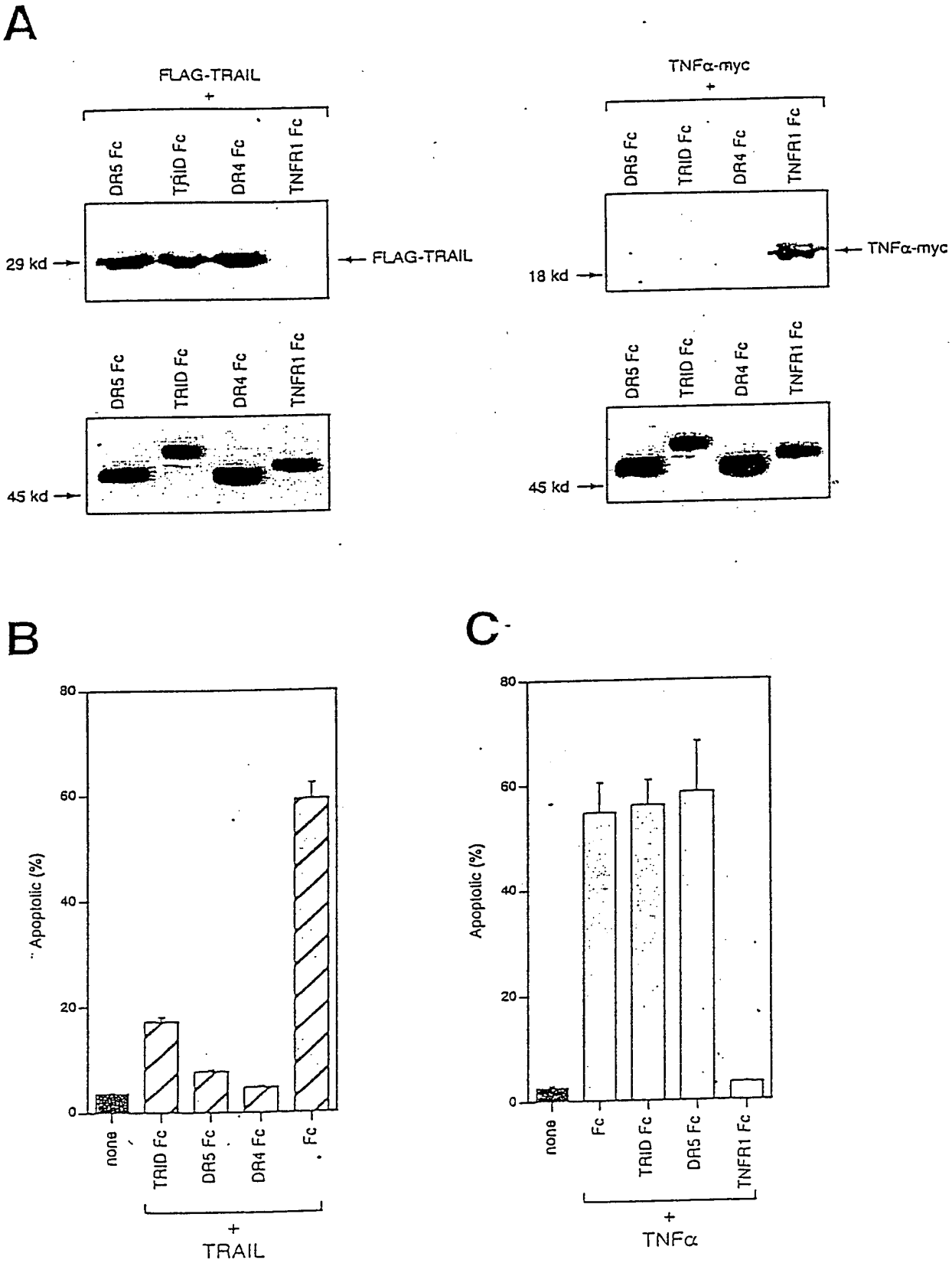

A
Apoptotic (%)
100
75
50
25
0
Vector
DR5
DR5Δ
TNFR1
MCF7 cells
B
Apoptotic (%)
100
75
50
25
0
Vector
DR5
DR5Δ
TNFR1
Hela cells
C
Apoptotic (%)
100
75
50
25
0
Vector
CrmA
FADD-DN
zVAD-fmk
Vector
+ DR5
D
HA-FADD
+
FLAG DR4
FLAG DR5
FLAG Fas
29 kd
FADD
myc-TRADD
+
FLAG DR5
FLAG DR4
FLAG TNFR1
45 kd
myc-TRADD
E
293 cells
Apoptotic (%)
50
40
30
20
10
0
Vector
CrmA
FLICE-DN
FLICE2-DN
Vector
CrmA
FLICE-DN
FLICE2-DN
+ DR5
+ TNFR1

Figure 6


A
FLAG-TRAIL
+
DR5 Fc
TRID Fc
DR4 Fc
TNFR1 Fc
29 kd
FLAG-TRAIL
45 kd
TNFα-myc
18 kd
TNFα-myc
B
Apoptotic (%)
80
60
40
20
0
none
TRID Fc
DR5 Fc
DR4 Fc
Fc
TRAIL
C
Apoptotic (%)
Fc
TNFR1 Fc
TNFα